

Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 1 167 519 A1**

(12)

EUROPEAN PATENT APPLICATION
published in accordance with Art. 158(3) EPC

(43) Date of publication:
02.01.2002 Bulletin 2002/01

(21) Application number: 00915459.2

(22) Date of filing: 10.04.2000

(51) Int Cl.7: **C12N 9/04**, C12N 15/53,
C12N 15/63, C12N 1/15,
C12N 1/19, C12N 1/21,
C12N 5/10, C12Q 1/32,
C12Q 1/54
// C12N9:04, C12R1:01

(86) International application number:
PCT/JP00/02322

(87) International publication number:
WO 00/61730 (19.10.2000 Gazette 2000/42)

(84) Designated Contracting States:
BE DE ES FR GB IT LU NL

(30) Priority: 08.04.1999 JP 10114399
18.01.2000 JP 2000009152

(71) Applicant: **Sode, Koji**
Tokyo 152-0013 (JP)

(72) Inventor: **Sode, Koji**
Tokyo 152-0013 (JP)

(74) Representative: **VOSSIUS & PARTNER**
Siebertstrasse 4
81675 München (DE)

(54) **GLUCOSE DEHYDROGENASE**

(57) Modified water-soluble glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme are provided wherein at least one amino acid residue is

replaced by another amino acid residue in a specific region. Modified water-soluble PQQGDHs of the present invention have improved thermal stability.

EP 1 167 519 A1

Description**TECHNICAL FIELD**

- 5 [0001] The present invention relates to the preparation of glucose dehydrogenases having pyrrolo-quinoline quinone as a coenzyme (PQQGDH) and their use for glucose assays.

BACKGROUND ART

- 10 [0002] Blood glucose is an important marker for diabetes. In the fermentative production using microorganisms, glucose levels are assayed for monitoring the process. Conventional glucose assays were based on enzymatic methods using a glucose oxidase (GOD) or glucose-6-phosphate dehydrogenase (G6PDH). However, GOD-based assays required addition of a catalase or peroxidase to the assay system in order to quantitate the hydrogen peroxide generated by glucose oxidation reaction. G6PDHs have been used for spectrophotometric glucose assays, in which case a coenzyme NAD(P) had to be added to the reaction system.

15 [0003] An object of the present invention is to provide a modified water-soluble PQQGDH with improved thermal stability.

DISCLOSURE OF THE INVENTION

- 20 [0004] We found that PQQGDHs with high stability are useful as novel enzymes alternative to the enzymes that have been used for enzymatic glucose assays. PQQGDHs are useful as recognition elements of glucose sensors because they have high oxidation activity for glucose and they are coenzyme-bound enzymes that require no oxygen as an electron acceptor.

- 25 [0005] PQQGDHs catalyze the reaction in which glucose is oxidized to produce gluconolactone. PQQGDHs include membrane-bound enzymes and water-soluble enzymes. Membrane-bound PQQGDHs are single peptide proteins having a molecular weight of about 87 kDa and widely found in various gram-negative bacteria. Water-soluble PQQGDHs have been identified in several strains of *Acinetobacter calcoaceticus* (Biosci. Biotech. Biochem. (1995), 59(8), 1548-1555), and their structural genes were cloned to show the amino acid sequences (Mol. Gen. Genet. (1989), 217: 30 430-436). The water-soluble PQQGDH derived from *A. calcoaceticus* is a homodimer having a molecular weight of about 50 kDa.

- [0006] Recently, a Dutch group made an X-ray crystal structure analysis of the water-soluble PQQGDH to show the higher-order structure of the enzyme (J. Mol. Biol., 289, 319-333 (1999). The crystal structure of the apo form of the soluble quinoprotein glucose dehydrogenase from *Acinetobacter calcoaceticus* reveals a novel internal conserved sequence repeat; A. Oubrie et al., The EMBO Journal, 18(19) 5187-5194 (1999), Structure and mechanism of soluble quinoprotein glucose dehydrogenase, A. Oubrie et al., PNAS, 96(21), 11787-11791 (1999), Active-site structure of the soluble quinoprotein glucose dehydrogenase complexed with methylhydrazine; A covalent cofactor-inhibitor complex, A. Oubrie et al.). These papers showed that the water-soluble PQQGDH is a β -propeller protein composed of six W-motifs (Fig. 7).

- 35 [0007] As a result of careful studies to develop a modified PQQGDH that can be applied to clinical tests or food analyses by improving the conventional water-soluble PQQGDH to increase the thermal stability, we succeeded in obtaining an enzyme with very high stability by introducing an amino acid change into a specific region of the water-soluble PQQGDH.

- 40 [0008] Accordingly, the present invention provides a modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein an amino acid residue corresponding to serine 231 or glutamine 209 or glutamate 210 or aspartate 420 or alanine 421 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* (hereinafter also referred to as the wild-type PQQGDH) is replaced by another amino acid residue. As used herein, the "modified glucose dehydrogenase" means a glucose dehydrogenase wherein at least one amino acid residue in a naturally occurring glucose dehydrogenase is replaced by another amino acid residue. The amino acid numbering herein starts from the initiator methionine as the +1 position.

- 45 [0009] The present invention also provides a modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein at least one amino acid residue is replaced by another amino acid residue in one or more regions selected from the group consisting of the regions defined by residues 48-53, 60-62, 69-71, 79-82, 91-101, 110-115, 127-135, 147-150, 161-169, 177-179, 186-221, 227-244, 250-255, 261-263, 271-275, 282-343, 349-377, 382-393, 50 400-403, 412-421, 427-432, 438-441 and 449-468 in the amino acid sequence shown as SEQ ID NO: 1, characterized in that it has higher thermal stability than that of the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus*. Preferably, the modified PQQGDH of the present invention has a residual activity that is higher than the residual activity of the wild-type PQQGDH by 10% or more, more preferably 20% or more, still more preferably 30% or more after heat

treatment at 50°C for 10 minutes. Preferably, the modified PQQGDH of the present invention has a heat inactivation half-life that is longer than the heat inactivation half-life of the wild-type PQQGDH by 5 minutes or more, more preferably 15 minutes or more at 55°C. In especially preferred modified PQQGDHs of the present invention, at least one amino acid residue is replaced by another amino acid residue in the region defined by residues 227-244, 186-221 or 412-421 in the amino acid sequence shown as SEQ ID NO: 1. In still more preferred modified PQQGDHs of the present invention, serine 231 is replaced by an amino acid residue selected from the group consisting of lysine, asparagine, aspartate, histidine, methionine, leucine and cysteine, or glutamine 209 is replaced by lysine, or glutamate 210 is replaced by lysine, or aspartate 420 is replaced by lysine, or alanine 421 is replaced by aspartate in the amino acid sequence shown as SEQ ID NO: 1.

[0010] In another aspect, modified PQQGDHs of the present invention comprise the sequence:

Asn Leu Asp Gly Xaa231 Ile Pro Lys Asp Asn Pro Ser Phe Asn
Gly Val Val Ser

wherein Xaa231 represents a natural amino acid residue other than Ser;
or the sequence:

Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
Gln Ala Gln His Thr Pro Thr Gln Xaa209 Xaa210 Leu Asn Gly
Lys Asp Tyr His Thr Tyr Met Gly

wherein Xaa209 and Xaa210 represent any natural amino acid residue, provided that when Xaa209 represents Gln, Xaa 210 does not represent Glu;
or the sequence:

Pro Thr Tyr Ser Thr Thr Tyr Asp Xaa420 Xaa421

wherein Xaa420 and Xaa421 represent any natural amino acid residue, provided that when Xaa420 represents Asp, Xaa421 does not represent Ala.

[0011] The present invention also provides a gene encoding any of the modified glucose dehydrogenases described above, a vector containing said gene and a transformant containing said gene, as well as a glucose assay kit and a glucose sensor comprising a modified glucose dehydrogenase of the present invention.

[0012] Enzyme proteins of modified PQQGDHs of the present invention have high thermal stability and high oxidation activity for glucose so that they can be applied to highly sensitive and highly selective glucose assays. Especially, they are expected to provide the advantages that the enzymes can be produced at high yield with less inactivation during preparation/purification; the enzymes can be easily stored because of their high stability in solutions; the enzymes can be used to prepare an assay kit or an enzyme sensor with less inactivation; and the assay kit or enzyme sensor prepared with the enzymes has excellent storage properties because of the high thermal stability.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013]

FIG. 1 shows the structure of the plasmid pGB2 used in the present invention.

FIG. 2 shows a scheme for preparing a mutant gene encoding a modified enzyme of the present invention.

FIG. 3 shows thermal stability of a modified enzyme of the present invention.

FIG. 4 shows substrate specificities of modified enzymes of the present invention.

FIG. 5 shows a glucose assay using a modified PQQGDH of the present invention.

FIG. 6 shows a calibration curve of an enzyme sensor using a modified PQQGDH of the present invention.

FIG. 7 shows the topology of a water-soluble GDH (Oubrie et al., Fig. 4).

THE MOST PREFERRED EMBODIMENTS OF THE INVENTIONStructure of modified PQQGDHs

5 [0014] We introduced random mutations into the coding region of the gene encoding the water-soluble PQQGDH by error-prone PCR to construct a library of water-soluble PQQGDHs carrying amino acid changes. These genes were transformed into *E. coli* and screened for the residual activity of the PQQGDHs after heat treatment to give a number of clones that express PQQGDHs with improved thermal stability.

[0015] Analysis of the nucleotide sequence of one of these clones showed that Ser 231 had been changed to Cys. When this amino acid residue was replaced by various other amino acid residues, mutant enzymes with higher thermal stability than that of the wild type water-soluble PQQGDH were obtained in every case.

10 [0016] The water-soluble PQQGDH has the structure of a β -propeller protein composed of six W-motifs. In the present invention, it was found that thermal stability is improved by replacing Ser 231 in the loop region defined by residues 227-244 by another amino acid residue. Then, site-specific mutations were introduced into other loop regions to try to improve the thermal stability. Mutant enzymes carrying Gln209Lys or Glu210Lys in the loop defined by residues 186-221 or Asp420Lys or Ala421Asp in the loop defined by residues 412-421 showed improved thermal stability.

15 [0017] Thus, it was demonstrated that water-soluble PQQGDHs with improved thermal stability can be constructed by introducing a proper change into a loop region according to the present invention. This is probably because the interaction between the loop regions connecting W-motifs contributes to the stabilization of the structure of the β -propeller protein in water-soluble PQQGDHs. The residues Ser231, Gln209, Gly210, Asp420 and Ala421 shown above are only illustrative but not limiting the present invention. The present invention first showed in the art that thermal stability of PQQGDHs can be improved by introducing a change into a specific site of the structural gene in a loop region, thereby providing here a methodology for improving thermal stability of PQQGDHs.

20 [0018] Modified PQQGDHs of the present invention are characterized in that they contain an amino acid residue change in a specific region in the amino acid sequence of the wild-type PQQGDH shown as SEQ ID NO: 1. Accordingly, the present invention provides a modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein at least one amino acid residue is replaced by another amino acid residue in one or more regions selected from the group consisting of the regions defined by residues 48-53, 60-62, 69-71, 79-82, 91-101, 110-115, 127-135, 147-150, 161-169, 177-179, 186-221, 227-244, 250-255, 261-263, 271-275, 282-343, 349-377, 382-393, 400-403, 30 412-421, 427-432, 438-441 and 449-468 in the amino acid sequence shown as SEQ ID NO: 1.

[0019] In preferred modified PQQGDHs of the present invention, at least one amino acid residue is replaced by another amino acid residue in the region defined by residues 227-244, 186-221 or 412-421 in the amino acid sequence shown as SEQ ID NO: 1. In especially preferred modified PQQGDHs of the present invention, serine 231 is replaced by an amino acid residue selected from the group consisting of lysine, asparagine, aspartate, histidine, methionine, leucine and cysteine, or glutamine 209 is replaced by lysine, or glutamate 210 is replaced by lysine, or aspartate 420 is replaced by lysine, or alanine 421 is replaced by aspartate in the amino acid sequence shown as SEQ ID NO: 1.

35 [0020] In another aspect, modified PQQGDHs of the present invention comprise the sequence:

40 Asn Leu Asp Gly Xaa231 Ile Pro Lys Asp Asn Pro Ser Phe Asn
Gly Val Val Ser

wherein Xaa231 represents a natural amino acid residue other than Ser;
45 or the sequence:

Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
50 Gln Ala Gln His Thr Pro Thr Gln Xaa209 Xaa210 Leu Asn Gly
Lys Asp Tyr His Thr Tyr Met Gly

55 wherein Xaa209 and Xaa210 represent any natural amino acid residue, provided that when Xaa209 represents Gln, Xaa 210 does not represent Glu;
or the sequence:

Pro Thr Tyr Ser Thr Thr Tyr Asp Xaa420 Xaa421

wherein Xaa420 and Xaa421 represent any natural amino acid residue, provided that when Xaa420 represents Asp, Xaa 421 does not represent Ala.

[0021] In modified glucose dehydrogenases of the present invention, other amino acid residues may be partially deleted or substituted or other amino acid residues may be added so far as glucose dehydrogenase activity is retained. Various techniques for such deletion, substitution or addition of amino acid residues are known in the art as described in Sambrook et al., "Molecular Cloning: A Laboratory Manual", Second Edition, 1989, Cold Spring Harbor Laboratory Press, New York, for example. Those skilled in the art can readily test whether or not a glucose dehydrogenase containing such deletion, substitution or addition has a desired glucose dehydrogenase activity according to the teaching herein. Those skilled in the art can also predict a region having a loop structure in water-soluble PQQGDHs derived from other bacteria according to the teaching herein and replace an amino acid residue in this region to obtain modified glucose dehydrogenases with improved thermal stability. Particularly, an amino acid residue corresponding to serine 231, glutamine 209, glutamate 210, aspartate 420 or alanine 421 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* can be readily identified by comparing the primary structures of proteins in alignment, so that modified glucose dehydrogenases can be obtained by replacing such a residue by another amino acid residue according to the present invention. These modified glucose dehydrogenases are also within the scope of the present invention.

Process for preparing modified PQQGDHs

[0022] The sequence of the gene encoding the wild-type water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is defined by SEQ ID NO: 2.

[0023] Genes encoding modified PQQGDHs of the present invention can be constructed by replacing the nucleotide sequence encoding an amino acid residue occurring in a loop region as described above in the gene encoding the wild-type water-soluble PQQGDH by the nucleotide sequence encoding an amino acid residue to be substituted. Various techniques for such site-specific nucleotide sequence substitution are known in the art as described in Sambrook et al., "Molecular Cloning: A Laboratory Manual", Second Edition, 1989, Cold Spring Harbor Laboratory Press, New York, for example. Thus obtained mutant gene is inserted into a gene expression vector (for example, a plasmid) and transformed into an appropriate host (for example, *E. coli*). A number of vector/host systems for expressing a foreign protein are known and various hosts such as bacteria, yeasts or cultured cells are suitable.

[0024] Random mutations are introduced by error-prone PCR into a target loop region to construct a gene library of modified water-soluble PQQGDHs carrying mutations in the loop region. These genes are transformed into *E. coli* to screen each clone for the thermal stability of the PQQGDH. Water-soluble PQQGDHs are secreted into the periplasmic space when they are expressed in *E. coli*, so that they can be easily assayed for enzyme activity using the *E. coli* cells. This library is heated at 60-70°C for about 30 minutes and then combined with glucose and a PMS-DCIP dye to visually determine the residual PQQGDH activity so that clones showing residual activity even after heat treatment are selected and analyzed for the nucleotide sequence to confirm the mutation.

[0025] Thus obtained transformed cells expressing modified PQQGDHs are cultured and harvested by centrifugation or other means from the culture medium, and then disrupted with a French press or osmotically shocked to release the periplasmic enzyme into the medium. The enzyme may be ultracentrifuged to give a water-soluble PQQGDH-containing fraction. Alternatively, the expressed PQQGDH may be secreted into the medium by using an appropriate host/vector system. The resulting water-soluble fraction is purified by ion exchange chromatography, affinity chromatography, HPLC and the like to prepare a modified PQQGDH of the present invention.

Method for assaying enzyme activity

[0026] PQQGDHs of the present invention associate with PQQ as a coenzyme in catalyzing the reaction in which glucose is oxidized to produce gluconolactone.

[0027] The enzyme activity can be assayed by using the color-developing reaction of a redox dye to measure the amount of PQQ reduced with PQQGDH-catalyzed oxidation of glucose. Suitable color-developing reagents include PMS (phenazine methosulfate)-DCIP (2,6-dichlorophenolindophenol), potassium ferricyanide and ferrocene, for example.

Thermal stability

[0028] Thermal stability of modified PQQGDHs of the present invention can be evaluated by incubating the enzyme of interest at a high temperature (for example, 55°C), sampling aliquots at regular intervals and assaying the enzyme

activity to monitor the decrease in the enzyme activity with time. Typically, thermal stability of an enzyme is expressed as a heat inactivation half-life, i.e. the time required for the enzyme activity to be reduced to 50% ($t_{1/2}$). Alternatively, thermal stability can also be expressed as the residual enzyme activity after heat treatment of the enzyme for a given period (the ratio of the activity after heat treatment to the activity before heat treatment).

[0029] Modified PQQGDHs of the present invention are characterized by higher thermal stability than that of the wild-type PQQGDH. Thus, they have the advantages that the enzymes can be produced at high yield with less inactivation during preparation/purification; the enzymes can be easily stored because of their high stability in solutions; the enzymes can be used to prepare an assay kit or an enzyme sensor with less inactivation; and the assay kit or enzyme sensor prepared with the enzymes has excellent storage properties because of the high thermal stability.

Glucose assay kit

[0030] The present invention also relates to a glucose assay kit comprising a modified PQQGDH according to the present invention. The glucose assay kit of the present invention comprises a modified PQQGDH according to the present invention in an amount enough for at least one run of assay. In addition to the modified PQQGDH according to the present invention, the kit typically comprises a necessary buffer for the assay, a mediator, standard glucose solutions for preparing a calibration curve and instructions. Modified PQQGDHs according to the present invention can be provided in various forms such as freeze-dried reagents or solutions in appropriate preservative solutions. Modified PQQGDHs according to the present invention are preferably provided in the form of a holoenzyme, though they may also be provided as an apoenzyme and converted into a holoenzyme before use.

Glucose sensor

[0031] The present invention also relates to a glucose sensor using a modified PQQGDH according to the present invention. Suitable electrodes include carbon, gold, platinum and the like electrodes, on which an enzyme of the present invention is immobilized by using a crosslinking agent; encapsulation in a polymer matrix; coating with a dialysis membrane; using a photo-crosslinkable polymer, an electrically conductive polymer or a redox polymer; fixing the enzyme in a polymer or adsorbing it onto the electrode with an electron mediator including ferrocene or its derivatives; or any combination thereof. Modified PQQGDHs of the present invention are preferably immobilized in the form of a holoenzyme on an electrode, though they may be immobilized as an apoenzyme and PQQ may be provided as a separate layer or in a solution. Typically, modified PQQGDHs of the present invention are immobilized on a carbon electrode with glutaraldehyde and then treated with an amine-containing reagent to block glutaraldehyde.

[0032] Glucose levels can be measured as follows. PQQ, CaCl_2 and a mediator are added to a thermostat cell containing a buffer and kept at a constant temperature. Suitable mediators include, for example, potassium ferricyanide and phenazine methosulfate. An electrode on which a modified PQQGDH of the present invention has been immobilized is used as a working electrode in combination with a counter electrode (e.g. a platinum electrode) and a reference electrode (e.g. an Ag/AgCl electrode). After a constant voltage is applied to the carbon electrode to reach a steady current, a glucose-containing sample is added to measure the increase in current. The glucose level in the sample can be calculated from a calibration curve prepared with glucose solutions at standard concentrations.

[0033] The disclosures of all the patents and documents cited herein are entirely incorporated herein as reference. The present application claims priority based on Japanese Patent Applications Nos. 1999-101143 and 2000-9152, the disclosure of which is entirely incorporated herein as reference.

[0034] The following examples further illustrate the present invention without, however, limiting the same thereto.

Example 1

Construction and screening of a mutant PQQGDH gene library:

[0035] The plasmid pGB2 was obtained by inserting the structural gene encoding the PQQGDH derived from *Acinetobacter calcoaceticus* into the multicloning site of the vector pTrc99A (Pharmacia) (Fig. 1). This plasmid was used as a template to introduce random mutations into the coding region by error-prone PCR. The PCR reaction was carried out in a solution having the composition shown in Table 1 under the conditions of 94°C for 3 minutes, 30 cycles of 94°C for 3 minutes, 50°C for 2 minutes and 72°C for 2 minutes, and finally 72°C for 10 minutes.

Table 1

TaqDNA polymerase (5U/ μ l)	0.5 μ l
Template DNA	1.0 μ l

Table 1 (continued)

Forward primer ABF	4.0 μ l
Reverse primer ABR	4.0 μ l
10 x Taq polymerase buffer	10.0 μ l
1M β -mercaptoethanol	1.0 μ l
DMSO	10.0 μ l
5 mM $MnCl_2$	10.0 μ l
10 mM dGTP	2.0 μ l
2 mM dATP	2.0 μ l
10 mM dCTP	2.0 μ l
10 mM dTTP	2.0 μ l
H ₂ O	51.5 μ l
	100.0 μ l

[0036] The resulting mutant water-soluble PQQGDH library was transformed into *E. coli* and each colony formed was transferred to a microtiter plate. After heating the plate at 60°C for about 30 minutes, glucose and PMS-DCIP were added and the residual PQQGDH activity was visually evaluated. A number of clones showing PQQGDH activity even after heat treatment were obtained.

[0037] One of these clones was randomly selected and analyzed for the nucleotide sequence to show that serine 231 had been changed to cysteine.

Example 2

Construction of modified PQQGDH genes:

[0038] Based on the structural gene of the PQQGDH derived from *Acinetobacter calcoaceticus* shown as SEQ ID NO: 2, the nucleotide sequence encoding serine 231, glutamine 209, aspartate 420 or alanine 421 was replaced by the nucleotide sequences encoding given amino acid residues by site-directed mutagenesis according to a standard method as shown in Fig. 2 using the plasmid pGB2. Table 2 shows the sequences of the synthetic oligonucleotide target primers used for mutagenesis. In Table 2, "S231D" means that serine 231 is replaced by aspartate, for example.

Table 2

5	S231D	5'-C CTT TGG AAT ATC TCC ATC AAG ATT TAA GC-3'
	S231H	5'-C CTT TGG AAT ATG TCC ATC AAG ATT TAA GC-3'
	S231K	5'-C CTT TGG AAT TTT TCC ATC AAG ATT TAA GC-3'
10	S231L	5'-C CTT TGG AAT CAT TCC ATC AAG ATT TAA GC-3'
	S231M	5'-C CTT TGG AAT AGT TCC ATC AAG ATT TAA GC-3'
15	S231N	5'-C CTT TGG AAT ATT TCC ATC AAG ATT TAA GC-3'
	I278F	5'-C AAT GAG GTT GAA TTC ATC GTC AGA G-3'
	Q209K	5'-C ACC ATT CAG TTC TTT TTG AGT TGG C-3'
20	E210K	5'-C ACC ATT CAG TTT TTG TTG AGT TGG C-3'
	D420K	5'-A CAT CGG TAC AGC TTT ATC ATA AGT AG-3'
25	A421D	5'-A CAT CGG TAC ATC GTC ATC ATA AGT AG-3'

[0039] A KpnI-HindIII fragment containing a part of the gene encoding the PQQGDH derived from *Acinetobacter calcoaceticus* was integrated into the vector plasmid pKF18k (Takara Shuzo Co., Ltd.) and used as a template. Fifty fmols of this template, 5 pmol of the selection primer attached to the Mutan™-Express Km Kit (Takara Shuzo Co., Ltd.) and 50 pmol of the phosphorylated target primer were mixed with the annealing buffer attached to the kit in an amount equivalent to 1/10 of the total volume (20 µl), and the mixture was heated at 100°C for 3 minutes to denature the plasmid into a single strand. The selection primer serves for reversion of dual amber mutations on the kanamycin-resistance gene of pKF18k. The mixture was placed on ice for 5 minutes to anneal the primers. To this mixture were added 3 µl of the extension buffer attached to the kit, 1 µl of T4 DNA ligase, 1 µl of T4 DNA polymerase and 5 µl of sterilized water to synthesize a complementary strand.

[0040] The synthetic strand was transformed into a DNA mismatch repair-deficient strain *E. coli* BMH71-18mutS and shake-cultured overnight to amplify the plasmid.

[0041] Then, the plasmid copies were extracted from the cultures and transformed into *E. coli* MV1184 and then extracted from the colonies. These plasmids were sequenced to confirm the introduction of the intended mutations. These fragments were substituted for the KpnI-HindIII fragment of the gene encoding the wild-type PQQGDH on the plasmid pGB2A to construct genes for modified PQQGDHs.

Example 3

Preparation of modified enzymes:

[0042] The gene encoding the wild-type or each modified PQQGDH was inserted into the multicloning site of an *E. coli* expression vector pTrc99A (Pharmacia), and the resulting plasmid was transformed into the *E. coli* strain DH5α. The transformant was shake-cultured at 37°C overnight on 450 ml of L medium (containing 50 µg/ml of ampicillin) in a Sakaguchi flask, and inoculated on 7 l of L medium containing 1 mM CaCl₂ and 500 µM PQQ. About 3 hours after starting cultivation, isopropyl thiogalactoside was added at a final concentration of 0.3 mM, and cultivation was further continued for 1.5 hours. The cultured cells were harvested from the medium by centrifugation (5,000 x g, 10 min, 4°C), and washed twice with a 0.85% NaCl solution. The collected cells were disrupted with a French press, and centrifuged (10,000 x g, 15 min, 4°C) to remove undisrupted cells. The supernatant was ultracentrifuged (160,500 x g (40,000 r.p.m.), 90 min, 4°C) to give a water-soluble fraction, which was used in the subsequent examples as a crude enzyme sample.

[0043] Thus obtained water-soluble fraction was further dialyzed against 10 mM phosphate buffer, pH 7.0 overnight. The dialyzed sample was adsorbed to a cation chromatographic column TSKgel CM-TOYOPEARL 650M (Tosoh Corp.),

which had been equilibrated with 10 mM phosphate buffer, pH 7.0. This column was washed with 750 ml of 10 mM phosphate buffer, pH 7.0 and then the enzyme was eluted with 10 mM phosphate buffer, pH 7.0 containing 0-0.2 M NaCl at a flow rate of 5 ml/min. Fractions having GDH activity were recovered and dialyzed against 10 mM MOPS-
 5 NaOH buffer, pH 7.0 overnight. Thus, an electrophoretically homogeneous modified PQQGDH protein was obtained. This was used in the subsequent examples as a purified enzyme sample.

Example 4

Assay of enzyme activity:

10 [0044] Enzyme activity was assayed by using PMS (phenazine methosulfate)-DCIP (2,6-dichlorophenolindophenol) in 10 mM MOPS-NaOH buffer (pH 7.0) to monitor changes in the absorbance of DCIP at 600 nm with a spectrophotometer and expressing the reaction rate of the enzyme as the rate of decrease in the absorbance. The enzyme activity for reducing 1 μ mol of DCIP in 1 minute was 1 U. The molar extinction coefficient of DCIP at pH 7.0 was 16.3 mM⁻¹.
 15

Example 5

Evaluation of thermal stability of crude enzyme samples:

20 [0045] Each of the crude enzyme samples of the wild-type and modified PQQGDHs obtained in Example 3 was converted into a holoenzyme in the presence of 1 μ M PQQ and 1 mM CaCl₂ for 1 hour or longer and then incubated at 55°C. Aliquots were sampled at regular intervals and rapidly cooled on ice. These samples were assayed for the enzyme activity by the method of Example 4 to determine the time required for reducing the activity to 50% ($t_{1/2}$).
 25 [0046] The results are shown in Table 3.

Table 3

	$t_{1/2}$ (min)
Wild type	10
S231K	95
S231L	16
S231D	25
S231C	50
S231M	14
S231H	15
S231N	50
I278F	25
Q209K	40
E210K	40
D420K	20
A421D	80

30 [0047] All the modified PQQGDHs of the present invention have a heat inactivation half-life at 55°C longer than that of the wild-type PQQGDH, showing that they have higher thermal stability than that of the wild-type PQQGDH.
 35

Example 6

Evaluation of thermal stability of purified enzyme samples:

50 [0048] The purified samples of the wild-type enzyme and the modified enzyme S231K obtained in Example 3 were measured for the heat inactivation half-life at 55°C in the same manner as in Example 5. The purified samples of the wild-type enzyme and the modified enzyme S231K had half-lives of 5 minutes and 41 minutes, respectively.

55 [0049] Then, each of the purified samples of the wild-type enzyme and the modified enzyme S231K obtained in Example 3 was converted into a holoenzyme in the presence of 1 μ M PQQ and 1 mM CaCl₂ for 1 hour or longer. Then, each sample was incubated at a given temperature in 10 mM MOPS buffer (pH 7.0) containing 1 μ M PQQ and 1 mM CaCl₂ for 10 minutes, and then rapidly cooled on ice. These samples were assayed for the enzyme activity by the

method of Example 4 to determine the residual activity relative to the activity before heat treatment.

[0050] The results are shown in Fig. 3. The modified enzyme S231K had higher activities than those of the wild-type enzyme at various temperatures of 40-62.5°C.

5 Example 7

Evaluation of enzyme activity:

[0051] The crude enzyme sample of the modified enzyme S231K obtained in Example 3 was converted into a holoenzyme in the presence of 1 μ M PQQ and 1 mM CaCl_2 for 1 hour or longer. A 187 μ l-aliquot was combined with 3 μ l of an activating reagent (prepared from 48 μ l of 6 mM DCIP, 8 μ l of 600 mM PMS and 16 μ l of 10 mM phosphate buffer, pH 7.0) and 10 μ l of glucose solutions at various concentrations, and assayed for the enzyme activity at room temperature by the method shown in Example 4. The K_m and V_{max} were determined by plotting the substrate concentration vs. enzyme activity. The S231K variant had a K_m value for glucose of about 20 mM and a V_{max} value of 3300 U/mg. The K_m value of the wild-type PQQGDH for glucose reported to date was about 20 mM with the V_{max} value being 2500-7000 U/mg depending on the measurement conditions. These results show that the modified PQQGDH S231K has high activity comparable to that of the wild-type PQQGDH.

20 Example 8

Evaluation of substrate specificity:

[0052] Crude samples of various modified enzymes were tested for substrate specificity. The substrates tested were glucose, 2-deoxy-D-glucose, mannose, allose, 3-o-methyl-D-glucose, galactose, xylose, lactose and maltose, and each sample was incubated with 20 mM of each substrate for 30 minutes in the presence of 1 μ M PQQ and 1 mM CaCl_2 and assayed for the enzyme activity in the same manner as in Example 7 to determine the relative activity to the activity for glucose. As shown in Fig. 4, all the modified enzymes of the present invention showed a similar substrate specificity to that of the wild-type enzyme.

30 Example 9

Glucose assay:

[0053] A modified PQQGDH was used for assaying glucose. The modified enzyme S231K was converted into a holoenzyme in the presence of 1 μ M PQQ and 1 mM CaCl_2 for 1 hour or longer, and assayed for the enzyme activity in the presence of glucose at various concentrations as well as 5 μ M PQQ and 10 mM CaCl_2 by the method described in Example 4 based on changes of the absorbance of DCIP at 600 nm. As shown in Fig. 5, the modified PQQGDH S231K can be used for assaying glucose in the range of 5 mM - 50 mM.

40 Example 10

Preparation and evaluation of an enzyme sensor:

[0054] Five units of the modified enzyme S231K was freeze-dried with 20 mg of carbon paste. After thorough mixing, the mixture was applied only on the surface of a carbon paste electrode preliminarily filled with about 40 mg of carbon paste and polished on a filter paper. This electrode was treated in 10 mM MOPS buffer (pH 7.0) containing 1% glutaraldehyde at room temperature for 30 minutes followed by 10 mM MOPS buffer (pH 7.0) containing 20 mM lysine at room temperature for 20 minutes to block glutaraldehyde. The electrode was equilibrated in 10 mM MOPS buffer (pH 7.0) at room temperature for 1 hour or longer and then stored at 4°C.

[0055] Thus prepared enzyme sensor was used to measure glucose levels. Fig. 6 shows the resulting calibration curve. Thus, the enzyme sensor having a modified PQQGDH of the present invention immobilized thereon could be used for assaying glucose in the range of 1 mM - 12 mM.

55 INDUSTRIAL APPLICABILITY

[0056] Modified PQQGDHs of the present invention have excellent thermal stability so that they are expected to provide the advantages that the enzymes can be produced at high yield with less inactivation during preparation/purification; the enzymes can be easily stored because of their high stability in solutions; the enzymes can be used to

EP 1 167 519 A1

prepare an assay kit or an enzyme sensor with less inactivation; and the assay kit or enzyme sensor prepared with the enzymes has excellent storage properties because of the high thermal stability.

5

10

15

20

25

30

35

40

45

50

55

Sequence Listing

5 <110> Sode, Koji
 <120> Glucose Dehydrogenase
 <130> YCT477
 10 <150> JP 11-101143
 <151> 1999-4-8
 <150> JP 2000-9152
 15 <151> 2000-1-18
 <160> 16
 <210> 1
 <211> 454
 20 <212> PRT
 <213> Acinetobacter calcoaceticus
 <400> 1
 25 Asp Val Pro Leu Thr Pro Ser Gln Phe Ala Lys Ala Lys Ser Glu Asn
 1 5 10 15
 Phe Asp Lys Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu
 30 20 25 30
 Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly
 35 40 45
 Lys Ile Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe
 35 50 55 60
 Gln Val Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu
 65 70 75 80
 40 Gly Phe Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Ile
 85 90 95
 Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
 100 105 110
 45 Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ser Thr Asp Thr Leu
 115 120 125
 Glu Lys Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His
 50 130 135 140
 Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
 145 150 155 160
 55 Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn

EP 1 167 519 A1

		165		170		175										
5	Gln	Ala	Gln	His	Thr	Pro	Thr	Gln	Gln	Glu	Leu	Asn	Gly	Lys	Asp	Tyr
		180		185		190										
	His	Thr	Tyr	Met	Gly	Lys	Val	Leu	Arg	Leu	Asn	Leu	Asp	Gly	Ser	Ile
10		195		200		205										
	Pro	Lys	Asp	Asn	Pro	Ser	Phe	Asn	Gly	Val	Val	Ser	His	Ile	Tyr	Thr
		210		215		220										
	Leu	Gly	His	Arg	Asn	Pro	Gln	Gly	Leu	Ala	Phe	Thr	Pro	Asn	Gly	Lys
15		225		230		235		240								
	Leu	Leu	Gln	Ser	Glu	Gln	Gly	Pro	Asn	Ser	Asp	Asp	Glu	Ile	Asn	Leu
		245		250		255										
20	Ile	Val	Lys	Gly	Gly	Asn	Tyr	Gly	Trp	Pro	Asn	Val	Ala	Gly	Tyr	Lys
		260		265		270										
	Asp	Asp	Ser	Gly	Tyr	Ala	Tyr	Ala	Asn	Tyr	Ser	Ala	Ala	Ala	Asn	Lys
		275		280		285										
25	Ser	Ile	Lys	Asp	Leu	Ala	Gln	Asn	Gly	Val	Lys	Val	Ala	Ala	Gly	Val
		290		295		300										
	Pro	Val	Thr	Lys	Glu	Ser	Glu	Trp	Thr	Gly	Lys	Asn	Phe	Val	Pro	Pro
30		305		310		315		320								
	Leu	Lys	Thr	Leu	Tyr	Thr	Val	Gln	Asp	Thr	Tyr	Asn	Tyr	Asn	Asp	Pro
		325		330		335										
35	Thr	Cys	Gly	Glu	Met	Thr	Tyr	Ile	Cys	Trp	Pro	Thr	Val	Ala	Pro	Ser
		340		345		350										
	Ser	Ala	Tyr	Val	Tyr	Lys	Gly	Gly	Lys	Lys	Ala	Ile	Thr	Gly	Trp	Glu
		355		360		365										
40	Asn	Thr	Leu	Leu	Val	Pro	Ser	Leu	Lys	Arg	Gly	Val	Ile	Phe	Arg	Ile
		370		375		380										
	Lys	Leu	Asp	Pro	Thr	Tyr	Ser	Thr	Thr	Tyr	Asp	Asp	Ala	Val	Pro	Met
45		385		390		395		400								
	Phe	Lys	Ser	Asn	Asn	Arg	Tyr	Arg	Asp	Val	Ile	Ala	Ser	Pro	Asp	Gly
		405		410		415										
50	Asn	Val	Leu	Tyr	Val	Leu	Thr	Asp	Thr	Ala	Gly	Asn	Val	Gln	Lys	Asp
		420		425		430										
	Asp	Gly	Ser	Val	Thr	Asn	Thr	Leu	Glu	Asn	Pro	Gly	Ser	Leu	Ile	Lys
		435		440		445										
55	Phe	Thr	Tyr	Lys	Ala	Lys										

450

5 <210> 2
 <211> 1612<212> DNA<213> Acinetobacter calcoaceticus
 <400> 2
 10 agctacttiti atgcaacaga gccitlcaga aatttagatt ttaalagatt cgtiaitcat 60
 cataalacaa atcalataga gaacicgtac aaacctitia ttagaggiti aaaaaitcic 120
 ggaaaaitti gacaaitiat aaggiggaca calgaalaaa caittaitgg claaaaitgc 180
 15 ttiailaagc gctgticagc tagtiacaci ctcagcatti gcigaigtic cictaacicc 240
 aictcaatit gclaaagcga aalcagagaa ctitigacaag aaagtiaic laictaaitc 300
 aaataagccg calgctitgt tatggggacc agalaalcaa atttgggtaa ctgagcgagc 360
 aacaggiaag aittciaagag ttaaitccaga gtcgggiagi gtaaaaacag titticaggt 420
 20 accagagatt gicaatgag ctgattggca gaaitggiti ttaggtititg ccttccatcc 480
 tgattitaaa aataatccit atactiatat ttcaggiaaca tttaaaaatc cgaaitctac 540
 agataaagaa tiaccgaacc aaacgaitat tctgtcttat acctataala aatcaacaga 600
 25 tacgticgag aagccagtcg aittattagc aggaattacct tcaicaaaag accalcagtc 660
 aggtcgtict gicatgggc cagatcaaaa gattiatat acgattggig accaagggcg 720
 taaccagctt gcttatitgt tcttgccaaa tcaagcaca cctacgccaa ctcaacaaga 780
 actgaalgtt aaagactatc acactiatat gggtaaagta ctacgcitaa aicttgaatg 840
 30 aagiatcca aaggataatc caagtittaa cggggigggt agccatait atacacttgg 900
 acatcgliaa cgcaggggt tagcattcac tccaaatgtt aaattattgc agtcigaaca 960
 aggcccaaac tctgacgatg aaaliaacct catgticaaa ggiggcaatt atgttggcc 1020
 35 gaatttagca ggittalaaag atgalatigg ctatgcttat gcaaatiait cagcagcagc 1080
 caataagica attaaggatt tagctcaaaa tggagtataa glagccgcag ggttccctgt 1140
 gacgaagaa tctgaatgga ctggtaaaaa ctitgtccca ccaataaaaa ctttatatac 1200
 40 cgticaagat acctacaact ataacgatcc aacttggga gagatgacct acatttgcig 1260
 gccaacagtt gcaccgtcat ctgcttatgt ctataagggc ggtaaaaaag caattacttg 1320
 ttgggaaaat acattaitgg tttcatctit aaaacgtgtt gicatitlcc giatiaagtt 1380
 agatccaact tatagcacta ctiaatgaga cgcgtaccg atgtitaaaga gcaacaaccg 1440
 45 tlatcgtgat gtgattgcaa gtccagaatg gaatgticta tatgtatlaa ctgatactgc 1500
 cggaaatgtc caaaaagatg atggctcagt aacaaatata ttagaaaacc caggatctct 1560
 caitaagtac acctataagg ctatgaata cagtcgcatl aaaaaccga tc 1612

50

<210> 3

<211> 18

55

<212> PRT

5 <213> Acinetobacter calcoaceticus
 <220>
 <222> 4
 <223> Xaa is any amino acid residue
 10 <400> 3
 Asn Leu Asp Gly Xaa Ile Pro Lys Asp Asn Pro Ser Phe Asn Gly Val
 1 5 10 15
 Val Ser
 15
 <210> 4
 <211> 36
 20 <212> PRT
 <213> Acinetobacter calcoaceticus
 <220>
 <222> 24
 25 <223> Xaa is any amino acid residue
 <222> 25
 <223> Xaa is any amino acid residue
 30 <400> 4
 Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn Gln
 1 5 10 15
 35 Ala Gln His Thr Pro Thr Gln Xaa Xaa Leu Asn Gly Lys Asp Tyr His
 20 25 30
 Thr Tyr Met Gly
 35
 40
 <210> 5
 <211> 10
 45 <212> PRT
 <213> Acinetobacter calcoaceticus
 <220>
 <222> 9
 50 <223> Xaa is any amino acid residue
 <222> 10
 <223> Xaa is any amino acid residue
 55 <400> 5

EP 1 167 519 A1

Pro Thr Tyr Ser Thr Thr Tyr Asp Xaa Xaa
1 5 10

5

<210> 6

<211> 30

10

<212> DNA

<213> Artificial Sequence

<220>

15

<223> primer for point mutation

<400> 6

cccttgggaat atctccatca agatttaagc 30

20

<210> 7

<211> 30

<212> DNA

25

<213> Artificial Sequence

<220>

<223> primer for point mutation

30

<400> 7

cccttgggaat atgtccatca agatttaagc 30

35

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

40

<220>

<223> primer for point mutation

<400> 8

45

cccttgggaat ttctccatca agatttaagc 30

50

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

55

<220>

<223> primer for point mutation

5 <400> 9
 cccttgggaat catlccatca agattlaagc 30

 10 <210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 15 <223> primer for point mutation
 <400> 10
 cccttgggaat agtlccatca agattlaagc 30

 20 <210> 11
 <211> 30
 <212> DNA
 25 <213> Artificial Sequence
 <220>
 <223> primer for point mutation
 30 <400> 11
 cccttgggaat attlccatca agattlaagc 30

 35 <210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 40 <220>
 <223> primer for point mutation
 <400> 12
 45 caatgagggtl gaatlcatcg tcagag 26

 50 <210> 13
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 55 <223> primer for point mutation

5 <400> 13
 gaccattcag ttctttttga gttagc 26

 10 <210> 14
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 15 <223> primer for point mutation
 <400> 14
 gaccattcag tttttgttga gttagc 26
 20
 <210> 15
 <211> 26
 <212> DNA
 25 <213> Artificial Sequence
 <220>
 <223> primer for point mutation
 30 <400> 15
 acatcggtac agcattatca taagtag 27

 35 <210> 16
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 40 <220>
 <223> primer for point mutation
 <400> 16
 45 acatcggtac atcgtatca taagtag 27

Claims

1. A modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein an amino acid residue corresponding to serine 231 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is replaced by another amino acid residue.
2. A modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein an amino acid residue corresponding to glutamine 209 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is

replaced by another amino acid residue.

3. A modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein an amino acid residue corresponding to glutamate 210 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is replaced by another amino acid residue.
4. A modified glucose dehydrogenase having pyrroloquinoline quinone as a coenzyme wherein an amino acid residue corresponding to aspartate 420 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is replaced by another amino acid residue.
5. A modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein an amino acid residue corresponding to alanine 421 in the water-soluble PQQGDH derived from *Acinetobacter calcoaceticus* is replaced by another amino acid residue.
6. A modified glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme wherein at least one amino acid residue is replaced by another amino acid residue in one or more regions selected from the group consisting of the regions defined by residues 48-53, 60-62, 69-71, 79-82, 91-101, 110-115, 127-135, 147-150, 161-169, 177-179, 186-221, 227-244, 250-255, 261-263, 271-275, 282-343, 349-377, 382-393, 400-403, 412-421, 427-432, 438-441 and 449-468 in the amino acid sequence shown as SEQ ID NO: 1, characterized in that it has higher thermal stability than that of the water-soluble glucose dehydrogenase derived from *Acinetobacter calcoaceticus*.
7. The modified glucose dehydrogenase of Claim 3 wherein at least one amino acid residue is replaced by another amino acid residue in the region defined by residues 227-244 in the amino acid sequence shown as SEQ ID NO: 1.
8. The modified glucose dehydrogenase of Claim 7 wherein serine 231 in the amino acid sequence shown as SEQ ID NO: 1 is replaced by another amino acid residue.
9. The modified glucose dehydrogenase of Claim 3 wherein at least one amino acid residue is replaced by another amino acid residue in the region defined by residues 186-221 in the amino acid sequence shown as SEQ ID NO: 1.
10. The modified glucose dehydrogenase of Claim 9 wherein an amino acid residue corresponding to glutamine 209 in the amino acid sequence shown as SEQ ID NO: 1 is replaced by another amino acid residue.
11. The modified glucose dehydrogenase of Claim 9 wherein an amino acid residue corresponding to glutamate 210 in the amino acid sequence shown as SEQ ID NO: 1 is replaced by another amino acid residue.
12. The modified glucose dehydrogenase of Claim 3 wherein at least one amino acid residue is replaced by another amino acid residue in the region defined by residues 412-421 in the amino acid sequence shown as SEQ ID NO: 1.
13. The modified glucose dehydrogenase of Claim 12 wherein an amino acid residue corresponding to aspartate 420 in the amino acid sequence shown as SEQ ID NO: 1 is replaced by another amino acid residue.
14. The modified glucose dehydrogenase of Claim 12 wherein an amino acid residue corresponding to alanine 421 in the amino acid sequence shown as SEQ ID NO: 1 is replaced by another amino acid residue.
15. A glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme comprising the sequence:

Asn Leu Asp Gly Xaa231 Ile Pro Lys Asp Asn Pro Ser Phe Asn
Gly Val Val Ser

wherein Xaa231 represents a natural amino acid residue other than Ser.
16. A glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme comprising the sequence:

Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
Gln Ala Gln His Thr Pro Thr Gln Xaa209 Xaa210 Leu Asn Gly
Lys Asp Tyr His Thr Tyr Met Gly

wherein Xaa209 and Xaa210 represent any natural amino acid residue, provided that when Xaa209 represents Gln, Xaa210 does not represent Glu.

17. A glucose dehydrogenase having pyrrolo-quinoline quinone as a coenzyme comprising the sequence:

Pro Thr Tyr Ser Thr Thr Tyr Asp Xaa420 Xaa421

wherein Xaa420 and Xaa421 represent any natural amino acid residue, provided that when Xaa420 represents Asp, Xaa421 does not represent Ala.

18. A gene encoding the modified glucose dehydrogenase of any one of Claims 1-17.

19. A vector comprising the gene of Claim 18.

20. A transformant comprising the gene of Claim 18.

21. The transformant of Claim 20 wherein the gene is integrated into the main chromosome.

22. A glucose assay kit comprising the modified glucose dehydrogenase of any one of Claims 1-17.

23. A glucose sensor comprising the modified glucose dehydrogenase of any one of Claims 1-17.

Fig. 1

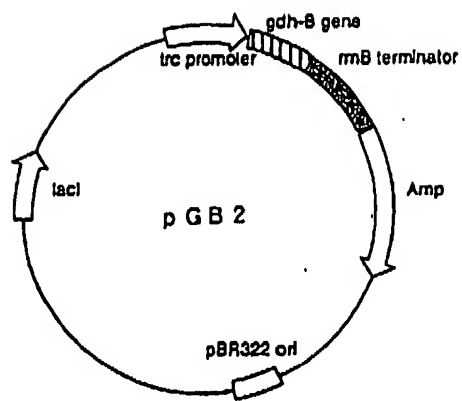


FIG. 2

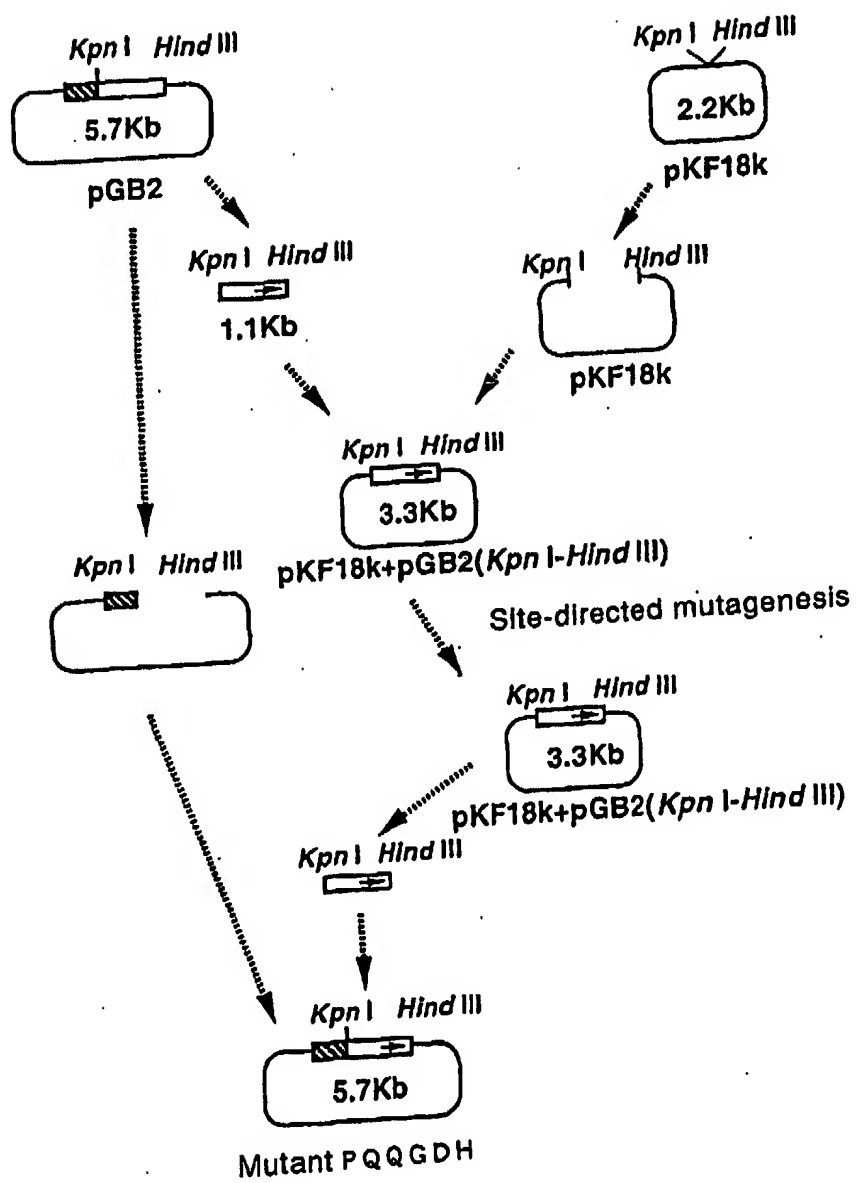


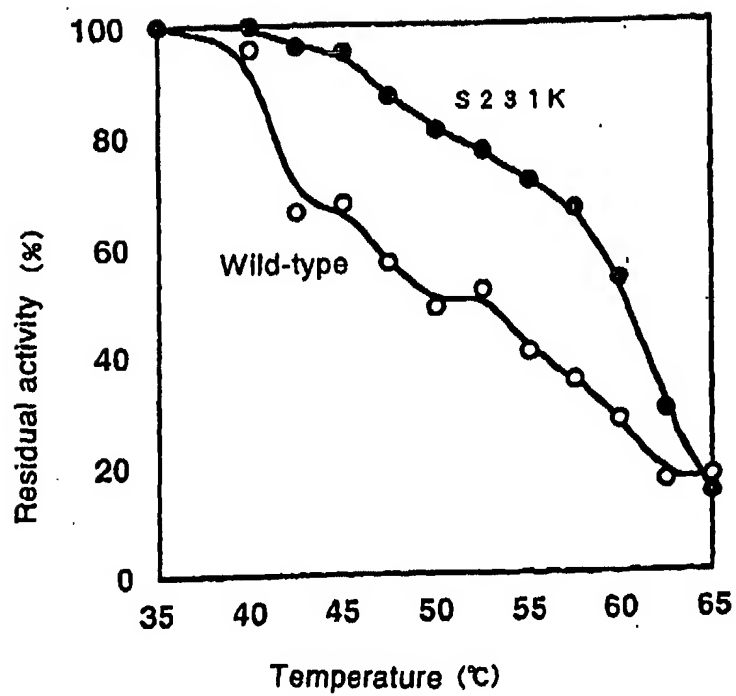
FIG. 3

FIG. 4

	Wild-type	S231K	S231C	S231L	S231D	S231N	S231M	S231H
Glucose	100	100	100	100	100	100	100	100
2-Deoxy-D-glucose	4	5	8	2	6	5	5	2
Mannose	13	10	8	9	13	12	9	12
Allose	47	43	46	38	62	61	43	57
3-o-Methyl-D-glucose	81	82	76	71	105	109	80	86
Galactose	11	15	14	12	20	18	10	17
Xylose	7	5	8	8	12	15	8	7
Lactose	61	59	69	54	73	66	56	56
Maltose	61	70	69	56	76	51	41	38

FIG. 5

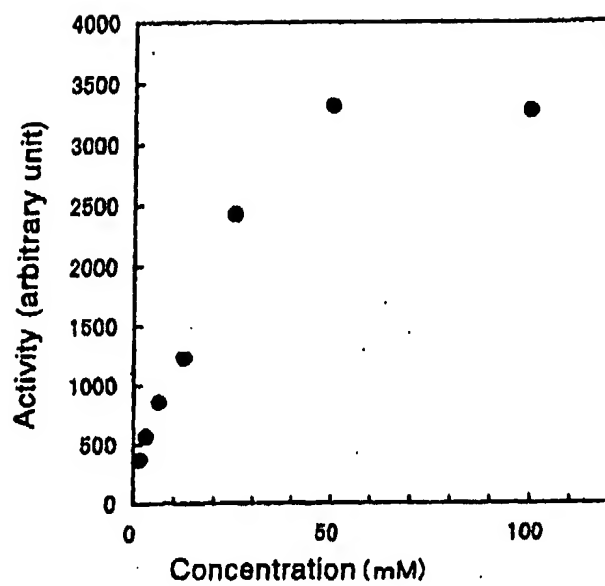


FIG. 6

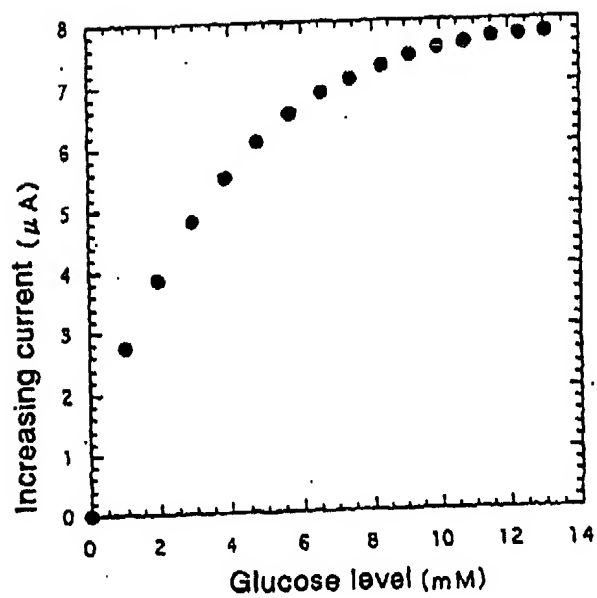
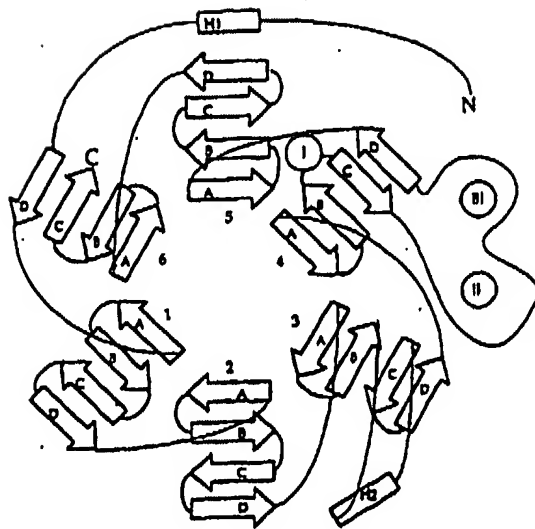


Fig. 7



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02322

A. CLASSIFICATION OF SUBJECT MATTER		
Int.Cl. ⁷ C12N 9/04, 15/53, 15/63, 1/15, 1/19, 1/21, 5/10, C12Q 1/32, 1/54 /(C12N 9/04, C12R 1:01)		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) Int.Cl. ⁷ C12N 9/04, 15/53, 15/63-869, 1/14-21, 5/10-28, C12Q 1/32, 1/54		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPI/L (DIALOG), BIOSIS (DIALOG), MEDLINE, JICST FILE (JOIS), CA (STN), REGISTRY (STN), GenBank/EMBL/GeneSeq, SwissProt/PIR/GeneSeq		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	JP, 11-243949, A (TOYOBO CO., LTD.), 14 September, 1999 (14.09.99) (Family: none)	1-23
P, X	IGARASHI, S. et al. "Construction and characterization of mutant water-soluble PQQ glucose dehydrogenases with altered K(m) values--site-directed mutagenesis studies on the putative active site.", Biochem. Biophys. Res. Commun. (1999, Nov.) Vol. 264, No. 3, pp. 820-824	1-23
Y	CLETON-JANSEN, A.-M., et al., "Cloning, Characterization and DNA sequencing of the gene encoding the Mr 50000 quinoprotein glucose dehydrogenases from Acinetobacter calcoaceticus.", Mol. Gen. Genet. (1989, Jun.) Vol. 217, No. 2-3, pp. 430-436	1-23
Y	US, 5114853, A (Amano Pharmaceutical Co., Ltd.), 19 May, 1992 (19.05.92) & JP, 2-86779, A & DE, 3931716, A	1-23
A	YOSHIDA, H. et al., "Engineering a chimeric pyrroloquinoline quinone glucose dehydrogenases:	1-23
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" documents referring to an oral disclosure, use, exhibition or other means "P" documents published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 27 April, 2000 (27.04.00)		Date of mailing of the international search report 16 May, 2000 (16.05.00)
Name and mailing address of the ISA/ Japanese Patent Office		Authorized officer
Facsimile No.		Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/02322

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	improvement of EDTA tolerance, thermal stability and substrate specificity.", Protein Eng. (1999, Jan.) Vol. 12, No. 1, pp. 63-70	
A	SODE, K. et al., "Increased production of recombinant pyrroloquinoline quinone (PQQ) glucose dehydrogenase by metabolically engineered Escherichia coli strain capable of PQQ biosynthesis.", J. Biotechnol. (1996, Aug.) Vol. 49, No. 1-3, pp. 239-243	1-23
A	EP, 78636, A (GENETICS INT., INC.), 11 May, 1983 (11.05.83) & US, 4545382, A & AU, 8289722, A & CA, 1212146, A	22-23

Form PCT/ISA/210 (continuation of second sheet) (July 1992)